

## SEQUENCE LISTING

<110> Zhou, Ming-Ming  
 <120> Methods of Identifying Modulators of the FGF Receptor  
 <130> 2459-1-002N  
 <140> 09/757415  
 <141> 2001-01-09  
 <150> 60/175867  
 <151> 2000-01-12  
 <160> 7  
 <170> PatentIn version 3.1  
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 <213> Homo sapien  
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 Met Gly Ser Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn  
 1 5 10 15  
 His Arg Asn Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu  
 20 25 30  
 Leu Gly Ser Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr  
 35 40 45  
 Thr Arg Lys Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg  
 50 55 60  
 Tyr Gly Tyr Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Arg Arg Cys  
 65 70 75 80  
 Gln Thr Gly Gln Gly Ile Phe Ala Phe Lys Cys Ala Arg Ala Glu Glu  
 85 90 95  
 Leu Phe Asn Met Leu Gln Glu Ile Met Gln Asn Asn Ser Ile Asn Val  
 100 105 110  
 Val Glu Glu Pro Val Val Glu Arg Asn Asn His Gln Thr Glu Leu Glu  
 115 120 125  
 Val Pro Arg Thr Pro Arg Thr Pro Thr Thr Pro Gly Phe Ala Ala Gln  
 130 135 140

Asn Leu Pro Asn Gly Tyr Pro Arg Tyr Pro Ser Phe Gly Asp Ala Ser  
145 150 155 160

Ser His Pro Ser Ser Arg His Pro Ser Val Gly Ser Ala Arg Leu Pro  
165 170 175

Ser Val Gly Glu Glu Ser Thr His Pro Leu Leu Val Ala Glu Glu Gln  
180 185 190

Val His Thr Tyr Val Asn Thr Thr Gly Val Gln Glu Glu Arg Lys Asn  
195 200 205

Arg Thr Ser Val His Val Pro Leu Glu Ala Arg Val Ser Asn Ala Glu  
210 215 220

Ser Ser Thr Pro Lys Glu Glu Pro Ser Ser Ile Glu Asp Arg Asp Pro  
225 230 235 240

Gln Ile Leu Leu Glu Pro Glu Gly Val Lys Phe Val Leu Gly Pro Thr  
245 250 255

Pro Val Gln Lys Gln Leu Met Glu Lys Glu Lys Leu Glu Gln Leu Gly  
260 265 270

Arg Asp Gln Val Ser Gly Ser Gly Ala Asn Asn Thr Glu Trp Asp Thr  
275 280 285

Gly Tyr Asp Ser Asp Glu Arg Arg Asp Ala Pro Ser Val Asn Lys Leu  
290 295 300

Val Tyr Glu Asn Ile Asn Gly Leu Ser Ile Pro Ser Ala Ser Gly Val  
305 310 315 320

Arg Arg Gly Arg Leu Thr Ser Thr Ser Thr Ser Asp Thr Gln Asn Ile  
325 330 335

Asn Asn Ser Ala Gln Arg Arg Thr Ala Leu Leu Asn Tyr Glu Asn Leu  
340 345 350

Pro Ser Leu Pro Pro Val Trp Glu Ala Arg Lys Leu Ser Arg Asp Glu  
355 360 365

Asp Asp Asn Leu Gly Pro Lys Thr Pro Ser Leu Asn Gly Tyr His Asn  
370 375 380

Asn Leu Asp Pro Met His Asn Tyr Val Asn Thr Glu Asn Val Thr Val

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385              390              395              400

Pro Ala Ser Ala His Lys Ile Glu Tyr Ser Arg Arg Arg Asp Cys Thr
      405              410              415

Pro Thr Val Phe Asn Phe Asp Ile Arg Arg Pro Ser Leu Glu His Arg
      420              425              430

Gln Leu Asn Tyr Ile Gln Val Asp Leu Glu Gly Gly Ser Asp Ser Asp
      435              440              445

Asn Pro Gln Thr Pro Lys Thr Pro Thr Thr Pro Leu Pro Gln Thr Pro
      450              455              460

Thr Arg Arg Thr Glu Leu Tyr Ala Val Ile Asp Ile Glu Arg Thr Ala
      465              470              475              480

Ala Met Ser Asn Leu Gln Lys Ala Leu Pro Arg Asp Asp Gly Thr Ser
      485              490              495

Arg Lys Thr Arg His Asn Ser Thr Asp Leu Pro Met
      500              505

<210> 2
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<213> Mus musculus

<400> 2

Met Trp Gly Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
1      5      10      15

Thr Leu Cys Thr Ala Arg Pro Ala Pro Thr Leu Pro Glu Gln Ala Gln
      20      25      30

Pro Trp Gly Val Pro Val Glu Val Glu Ser Leu Leu Val His Pro Gly
      35      40      45

Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
      50      55      60

Asn Trp Leu Arg Asp Gly Val Gln Leu Val Glu Ser Asn Arg Thr Arg
      65      70      75      80

Ile Thr Gly Glu Glu Val Glu Val Arg Asp Ser Ile Pro Ala Asp Ser
      85      90      95

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Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr  
 100 105 110

Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp  
 115 120 125

Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr  
 130 135 140

Lys Pro Asn Arg Arg Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys  
 145 150 155 160

Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe  
 165 170 175

Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys  
 180 185 190

Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val  
 195 200 205

Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp  
 210 215 220

Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn  
 225 230 235 240

His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile  
 245 250 255

Leu Gln Ala Gly Leu Pro Ala Asn Glu Thr Val Ala Leu Gly Ser Asn  
 260 265 270

Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln  
 275 280 285

Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn  
 290 295 300

Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp  
 305 310 315 320

Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala  
 325 330 335

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His  
 340 345 350  
 Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val  
 355 360 365  
 Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala  
 370 375 380  
 Phe Leu Ile Ser Cys Met Leu Gly Ser Val Ile Ile Tyr Lys Met Lys  
 385 390 395 400  
 Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys  
 405 410 415  
 Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp  
 420 425 430  
 Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg  
 435 440 445  
 Leu Ser Ser Ser Gly Thr Pro Met Pro Ala Gly Val Ser Glu Tyr Glu  
 450 455 460  
 Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu  
 465 470 475 480  
 Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu  
 485 490 495  
 Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala  
 500 505 510  
 Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu  
 515 520 525  
 Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile  
 530 535 540  
 Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile  
 545 550 555 560  
 Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg  
 565 570 575  
 Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu

580	585	590
Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala		
595	600	605
Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu		
610	615	620
Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala		
625	630	635 640
Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys		
	645	650 655
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu		
	660	665 670
Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val		
	675	680 685
Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val		
	690	695 700
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp		
705	710	715 720
Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys		
	725	730 735
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu		
	740	745 750
Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Ser Gln Glu Tyr Leu Asp		
	755	760 765
Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg		
	770	775 780
Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro		
785	790	795 800
Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Thr Gln Leu Ala Asn		
	805	810 815
Ser Gly Leu Lys Arg Arg		
	820	

<210> 3  
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<212> PRT  
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<400> 3

His Ser Gln Met Ala Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg  
1 5 10 15

Arg Gln Val Thr Val Ser  
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<210> 4  
<211> 11  
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<220>  
<223> Tyrosine phosphorylation peptide

<220>  
<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> Xaa is a phosphotyrosine

<400> 4

Leu Val Ile Ala Gly Asn Pro Ala Xaa Arg Ser  
1 5 10

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<211> 16  
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<223> Consensus sequence

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<220>  
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<400> 5

Val Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Leu Xaa Arg Xaa Val Xaa Val  
1 5 10 15

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<212> PRT  
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<223> Motif

<220>  
<221> MISC\_FEATURE  
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<223> Xaa can be any amino acid

<220>  
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<400> 6

Asn Pro Xaa Xaa  
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<210> 7  
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<212> PRT  
<213> Artificial Sequence

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<223> Synthetic peptide derived from the TrKA receptor  
  
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<400> 7

His Ile Ile Glu Asn Pro Gln Xaa Phe Ser Asp Ala  
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